



SEQUENCE LISTING

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National Research Council of Canada

<120> Lipopolysaccharide alpha-2,3 Sialyltransferase of
Campylobacter jejuni and Its Uses

<130> 019633-000912US

<140> US 10/799,016
<141> 2004-03-11

<150> US 60/078,891
<151> 1998-03-20

<150> US 09/272,960
<151> 1999-03-18

<150> US 10/058,636
<151> 2002-01-29

<160> 8

<170> PatentIn Ver. 2.0

<210> 1
<211> 1293
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(1293)
<223> Campylobacter jejuni OH4384 cst-I gene
alpha2,3-sialyltransferase

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Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met
1 5 10 15
caa aat ata atc ata gca gga aat gga cct agc cta aaa aat att aat 96
Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn
20 25 30
tat aaa aga ctg cct aga gaa tat gat gtt ttt agg tgt aac cag ttt 144
Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe
35 40 45
tat ttt gaa gat aag tat tat tta gga aaa aag att aaa gca gta ttt 192
Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe
50 55 60
ttt aat cct ggt gtc ttt tta caa cag tat cac act gca aaa caa ctt 240
Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu
65 70 75 80

| | |
|---|-----|
| ata cta aaa aat gag tat gaa ata aaa aat att ttt tgc tct aca ttt | 288 |
| Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe | |
| 85 90 95 | |
| aat tta cct ttt att gaa agc aat gat ttt tta cat caa ttt tat aat | 336 |
| Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn | |
| 100 105 110 | |
| ttt ttc ccc gat gca aaa ctt ggc tat gaa gtt att gaa aac ctt aaa | 384 |
| Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys | |
| 115 120 125 | |
| gaa ttt tat gct tat ata aaa tac aat gaa att tat ttc aat aaa aga | 432 |
| Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg | |
| 130 135 140 | |
| att act tcg ggc gtc tat atg tgt gca att gct att gca tta gga tat | 480 |
| Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr | |
| 145 150 155 160 | |
| aaa acc atc tat tta tgt ggc att gat ttt tat gaa gga gat gtt att | 528 |
| Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile | |
| 165 170 175 | |
| tat cct ttt gaa gct atg agt aca aat ata aaa aca atc ttt cct gga | 576 |
| Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly | |
| 180 185 190 | |
| ata aaa gat ttc aaa cct tca aat tgt cat tct aag gaa tac gat ata | 624 |
| Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile | |
| 195 200 205 | |
| gaa gca tta aaa ttg tta aaa tca ata tac aaa gtt aat atc tac gca | 672 |
| Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala | |
| 210 215 220 | |
| ttg tgt gat gat tct att ttg gca aat cat ttt cct tta tca att aat | 720 |
| Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn | |
| 225 230 235 240 | |
| att aat aac aat ttc act tta gaa aat aag cat aat aat tct ata aat | 768 |
| Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn | |
| 245 250 255 | |
| gat att tta ttg act gat aat act cct ggc gta agt ttt tat aaa aat | 816 |
| Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn | |
| 260 265 270 | |
| caa ctt aaa gct gat aat aaa att atg ctt aat ttt tat aat att ctt | 864 |
| Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu | |
| 275 280 285 | |
| cat tct aaa gat aat tta att aaa ttt tta aac aaa gaa att gcg gta | 912 |
| His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val | |
| 290 295 300 | |
| tta aaa aaa caa acc act caa cga gct aaa gca aga atc caa aac cat | 960 |
| Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His | |
| 305 310 315 320 | |

cta tcc tat aaa cta gga caa gct ttg att ata aat tct aaa agt gta 1008
 Leu Ser Tyr Lys Leu Gly Gln Ala Leu Ile Ile Asn Ser Lys Ser Val
 325 330 335

tta ggt ttt tta tct tta cct ttt ata ata tta agt atc gtt att tca 1056
 Leu Gly Phe Leu Ser Leu Pro Phe Ile Ile Leu Ser Ile Val Ile Ser
 340 345 350

cat aaa caa gaa caa aag gct tat aaa ttt aaa gta aag aaa aat cca 1104
 His Lys Gln Glu Gln Lys Ala Tyr Lys Phe Lys Val Lys Lys Asn Pro
 355 360 365

aat tta gct tta cct cct tta gaa act tat cct gat tat aat gaa gct 1152
 Asn Leu Ala Leu Pro Pro Leu Glu Thr Tyr Pro Asp Tyr Asn Glu Ala
 370 375 380

tta aaa gaa aaa gaa tgt ttt act tat aaa tta gga gaa gaa ttt ata 1200
 Leu Lys Glu Lys Glu Cys Phe Thr Tyr Lys Leu Gly Glu Glu Phe Ile
 385 390 395 400

aaa gct ggt aag aat tgg tat ggg gag ggg tat atc aaa ttt ata ttc 1248
 Lys Ala Gly Lys Asn Trp Tyr Gly Glu Gly Tyr Ile Lys Phe Ile Phe
 405 410 415

aaa gat gtt cct agg ttg aag aga gag ttt gag aaa ggg gaa taa 1293
 Lys Asp Val Pro Arg Leu Lys Arg Glu Phe Glu Lys Gly Glu
 420 425 430

<210> 2

<211> 430

<212> PRT

<213> Campylobacter jejuni

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Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met
 1 5 10 15

Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn
 20 25 30

Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe
 35 40 45

Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe
 50 55 60

Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu
 65 70 75 80

Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe
 85 90 95

Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn
 100 105 110

Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys
 115 120 125

Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg
 130 135 140

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Ser | Gly | Val | Tyr | Met | Cys | Ala | Ile | Ala | Ile | Ala | Leu | Gly | Tyr | 145 | 150 | 155 | 160 |
| Lys | Thr | Ile | Tyr | Leu | Cys | Gly | Ile | Asp | Phe | Tyr | Glu | Gly | Asp | Val | Ile | 165 | 170 | | 175 |
| Tyr | Pro | Phe | Glu | Ala | Met | Ser | Thr | Asn | Ile | Lys | Thr | Ile | Phe | Pro | Gly | 180 | 185 | | 190 |
| Ile | Lys | Asp | Phe | Lys | Pro | Ser | Asn | Cys | His | Ser | Lys | Glu | Tyr | Asp | Ile | 195 | 200 | | 205 |
| Glu | Ala | Leu | Lys | Leu | Leu | Lys | Ser | Ile | Tyr | Lys | Val | Asn | Ile | Tyr | Ala | 210 | 215 | | 220 |
| Leu | Cys | Asp | Asp | Ser | Ile | Leu | Ala | Asn | His | Phe | Pro | Leu | Ser | Ile | Asn | 225 | 230 | 235 | 240 |
| Ile | Asn | Asn | Asn | Phe | Thr | Leu | Glu | Asn | Lys | His | Asn | Asn | Ser | Ile | Asn | 245 | 250 | | 255 |
| Asp | Ile | Leu | Leu | Thr | Asp | Asn | Thr | Pro | Gly | Val | Ser | Phe | Tyr | Lys | Asn | 260 | 265 | | 270 |
| Gln | Leu | Lys | Ala | Asp | Asn | Lys | Ile | Met | Leu | Asn | Phe | Tyr | Asn | Ile | Leu | 275 | 280 | | 285 |
| His | Ser | Lys | Asp | Asn | Leu | Ile | Lys | Phe | Leu | Asn | Lys | Glu | Ile | Ala | Val | 290 | 295 | 300 | |
| Leu | Lys | Lys | Gln | Thr | Thr | Gln | Arg | Ala | Lys | Ala | Arg | Ile | Gln | Asn | His | 305 | 310 | 315 | 320 |
| Leu | Ser | Tyr | Lys | Leu | Gly | Gln | Ala | Leu | Ile | Ile | Asn | Ser | Lys | Ser | Val | 325 | 330 | | 335 |
| Leu | Gly | Phe | Leu | Ser | Leu | Pro | Phe | Ile | Ile | Leu | Ser | Ile | Val | Ile | Ser | 340 | 345 | | 350 |
| His | Lys | Gln | Glu | Gln | Lys | Ala | Tyr | Lys | Phe | Lys | Val | Lys | Lys | Asn | Pro | 355 | 360 | 365 | |
| Asn | Leu | Ala | Leu | Pro | Pro | Leu | Glu | Thr | Tyr | Pro | Asp | Tyr | Asn | Glu | Ala | 370 | 375 | 380 | |
| Leu | Lys | Glu | Lys | Glu | Cys | Phe | Thr | Tyr | Lys | Leu | Gly | Glu | Glu | Phe | Ile | 385 | 390 | 395 | 400 |
| Lys | Ala | Gly | Lys | Asn | Trp | Tyr | Gly | Glu | Gly | Tyr | Ile | Lys | Phe | Ile | Phe | 405 | 410 | | 415 |
| Lys | Asp | Val | Pro | Arg | Leu | Lys | Arg | Glu | Phe | Glu | Lys | Gly | Glu | | | 420 | 425 | | 430 |

<210> 3

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ18F 5' primer

<400> 3

cttaggaggt catatgacaa ggactagaat ggaaaatgaa c

41

<210> 4

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ40R 3' primer

<400> 4

cctaggtcga ctcattagtgt gtgatgggtgg tgaatgtccc ctttctcaaa ctctctcttc 60

<210> 5

<211> 231

<212> PRT

<213> Haemophilus influenzae

<220>

<223> Haemophilus influenzae Rd putative open reading
frame (ORF)

<400> 5

Met Gln Leu Ile Lys Asn Asn Glu Tyr Glu Tyr Ala Asp Ile Ile Leu
1 5 10 15

Ser Ser Phe Val Asn Leu Gly Asp Ser Glu Leu Lys Lys Ile Lys Asn
20 25 30

Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn
35 40 45

Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu
50 55 60

Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val
65 70 75 80

Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu
85 90 95

Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys
100 105 110

Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser
115 120 125

Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly
130 135 140

Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe
145 150 155 160

Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys
165 170 175

Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys
 180 185 190

Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe
 195 200 205

Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala
 210 215 220

Leu Lys Ser Arg Lys Trp Asp
 225 230

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:6 His tail,
 (His)6, polyhistidine tag, six adjacent histidines,
 metal chelate affinity ligand

<400> 6

His His His His His His
 1 5

<210> 7

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:linker between
 two fusion protein domains

<400> 7

Gly Gly Gly His
 1

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TM-FLAG tag,
 epitope tag

<400> 8

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5